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DEC 18 2001RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,217DATE: 06/14/2001
TIME: 15:44:47Input Set : N:\Crf3\RULE60\09828217.txt
Output Set: N:\CRF3\06142001\I828217.raw

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: HIRANO, TOSHIO
6 KAISHO, TSUNEYASU
8 (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
9 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
11 (iii) NUMBER OF SEQUENCES: 2
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
15 P.C.
16 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 1400
17 (C) CITY: ARLINGTON
18 (D) STATE: VA
19 (E) COUNTRY: USA
20 (F) ZIP: 22202
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/828,217
C--> 30 (B) FILING DATE: 09-Apr-2001
31 (C) CLASSIFICATION:
40 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 09/182,563
35 (B) FILING DATE:
37 (A) APPLICATION NUMBER: PCT/JP94/01732
38 (B) FILING DATE: 14-OCT-1994
41 (A) APPLICATION NUMBER: JP 5-281622
42 (B) FILING DATE: 15-OCT-1993
44 (viii) ATTORNEY/AGENT INFORMATION:
45 (A) NAME: OBLON, NORMAN F.
46 (B) REGISTRATION NUMBER: 24,618
47 (C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
49 (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: 703-413-3000
51 (B) TELEFAX: 703-413-2220
54 (2) INFORMATION FOR SEQ ID NO: 1:
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 180 amino acids
58 (B) TYPE: amino acid
59 (C) STRANDEDNESS: single
60 (D) TOPOLOGY: linear
62 (ii) MOLECULE TYPE: peptide
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

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70	1	5	10	15
72	Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu			
73	20	25	30	
75	Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala			
76	35	40	45	
78	Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg			
79	50	55	60	
81	Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly			
82	65	70	75	80
84	Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met			
85	85	90	95	
87	Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys			
88	100	105	110	
90	Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln			
91	115	120	125	
93	Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu			
94	130	135	140	
96	Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser			
97	145	150	155	160
99	Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser			
100	165	170	175	
102	Ala Leu Leu Gln			
103	180			

105 (2) INFORMATION FOR SEQ ID NO: 2:

107 (i) SEQUENCE CHARACTERISTICS:

- 108 (A) LENGTH: 996 base pairs
- 109 (B) TYPE: nucleic acid
- 110 (C) STRANDEDNESS: double
- 111 (D) TOPOLOGY: linear

113 (ii) MOLECULE TYPE: cDNA to mRNA

118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

120	GTGGAATTCA TGGCATCTAC TTCTGTATGAC TATTGCAGAG TGCCCAGTGGAA AGACGGGGAT	60
122	AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG	120
124	GGGGTGCCTCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCCTT	180
126	CGGGCAGTGA TGGAGTGTG CAATGTCACC CATCTCCTGC AACAAAGAGCT GACCGAGGCC	240
128	CAGAAGGGCT TTCAGGATGT GGAGGCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC	300
130	CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGAA GGAGCTTGAG	360
132	GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG	420
134	AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAAGTACTA CCCCCAGCTCC	480
136	CAGGACTCCA GCTCCGCTGC GGCGCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT	540
138	CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGGAA GGTCCGTCCT GCTCGGCTTT	600
140	TCGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG	660
142	CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG	720
144	GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCCTCCCT CCAGAGCCTC	780
146	CCTCCGGACA ATGAGTCCCC CCTCTTGTCT CCCACCCCTGA GATTGGGCAT GGGGTGCGGT	840
148	GTGGGGGGCA TGTGCTGCCT GTTGTATGG GTTTTTTTG CGGGGGGGT TGCTTTTTC	900
150	TGGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCTTGAG GGAGAGCAAA AAAAAAA	960
152	AAAAAAAAAA AAAAAAAAA AAAGAATTCC ACCACA	996

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/828,217

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]